CRF Errors Corrected by the STIC Systems Branch

Serial Number: 10/070,099 ~~ENTERED~~

CRF Processing Date: 8/12/2002
Edited by: ___
Verified by: ___ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PCT10

```
RAW SEQUENCE LISTING                    DATE: 08/12/2002
PATENT APPLICATION:  US/10/070,099      TIME: 17:41:50

         Input Set : A:\PTO.AMC.txt
         Output Set: N:\CRF4\08122002\J070099.raw
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     3 <110> APPLICANT: Niederweis Dr., Michael
     4        Bossmann Dr., Stefan
     6 <120> TITLE OF INVENTION: Method for the Production of a Channel-forming Protein
     8 <130> FILE REFERENCE: 401172
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/070,099
C--> 11 <141> CURRENT FILING DATE: 2002-07-08
    13 <150> PRIOR APPLICATION NUMBER: DE 199 43 520.0
    14 <151> PRIOR FILING DATE: 1999-09-11
    16 <150> PRIOR APPLICATION NUMBER: DE 199 41 416.5
    17 <151> PRIOR FILING DATE: 1999-08-31
    19 <160> NUMBER OF SEQ ID NOS: 9
    21 <170> SOFTWARE: PatentIn Ver. 2.1
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 636
    25 <212> TYPE: DNA
    26 <213> ORGANISM: Mycobacterium smegmatis
    28 <220> FEATURE:
    29 <221> NAME/KEY: CDS
    30 <222> LOCATION: (1)..(636)
    31 <223> OTHER INFORMATION: mspA-Gene
    33 <400> SEQUENCE: 1
    34 atg aag gca atc agt cgg gtg ctg atc gcg atg gtt gca gcc atc gcg    48
    35 Met Lys Ala Ile Ser Arg Val Leu Ile Ala Met Val Ala Ala Ile Ala
    36  1               5                  10                  15
    38 gcg ctt ttc acg agc aca ggc acc tct cac gca ggc ctg gac aac gag    96
    39 Ala Leu Phe Thr Ser Thr Gly Thr Ser His Ala Gly Leu Asp Asn Glu
    40              20                  25                  30
    42 ctg agc ctc gtt gat ggc cag gac cgc acc ctc acc gtg cag cag tgg   144
    43 Leu Ser Leu Val Asp Gly Gln Asp Arg Thr Leu Thr Val Gln Gln Trp
    44          35                  40                  45
    46 gac acc ttc ctc aat ggt gtg ttc ccc ctg gac cgc aac cgt ctt acc   192
    47 Asp Thr Phe Leu Asn Gly Val Phe Pro Leu Asp Arg Asn Arg Leu Thr
    48      50                  55                  60
    50 cgt gag tgg ttc cac tcc ggt cgc gcc aag tac atc gtg gcc ggc ccc   240
    51 Arg Glu Trp Phe His Ser Gly Arg Ala Lys Tyr Ile Val Ala Gly Pro
    52  65                  70                  75                  80
    54 ggt gcc gac gag ttc gag ggc acg ctg gaa ctc ggc tac cag atc ggc   288
    55 Gly Ala Asp Glu Phe Glu Gly Thr Leu Glu Leu Gly Tyr Gln Ile Gly
    56              85                  90                  95
    58 ttc ccg tgg tcg ctg ggt gtg ggc atc aac ttc agc tac acc acc ccg   336
    59 Phe Pro Trp Ser Leu Gly Val Gly Ile Asn Phe Ser Tyr Thr Thr Pro
    60             100                 105                 110
    62 aac atc ctg atc gac gac ggt gac atc acc gct ccg ccg ttc ggc ctg   384
```

```
63 Asn Ile Leu Ile Asp Asp Gly Asp Ile Thr Ala Pro Pro Phe Gly Leu
64         115             120             125
66 aac tcg gtc atc acc ccg aac ctg ttc ccc ggt gtg tcg atc tcg gca    432
67 Asn Ser Val Ile Thr Pro Asn Leu Phe Pro Gly Val Ser Ile Ser Ala
68         130             135             140
70 gat ctg ggc aac ggc ccc ggc atc cag gaa gtc gca acg ttc tcg gtc    480
71 Asp Leu Gly Asn Gly Pro Gly Ile Gln Glu Val Ala Thr Phe Ser Val
72 145             150             155             160
74 gac gtc tcc ggc gcc gag ggt ggc gtg gcc gtg tcg aac gcc cac ggc    528
75 Asp Val Ser Gly Ala Glu Gly Gly Val Ala Val Ser Asn Ala His Gly
76             165             170             175
78 acc gtg acc ggt gcg gcc ggc ggt gtg ctg ctg cgt ccg ttc gcc cgc    576
79 Thr Val Thr Gly Ala Ala Gly Gly Val Leu Leu Arg Pro Phe Ala Arg
80             180             185             190
82 ctg atc gcc tcg acc ggt gac tcg gtc acc acc tac ggc gaa ccc tgg    624
83 Leu Ile Ala Ser Thr Gly Asp Ser Val Thr Thr Tyr Gly Glu Pro Trp
84             195             200             205
86 aac atg aac tga                                                    636
87 Asn Met Asn
88     210
91 <210> SEQ ID NO: 2
92 <211> LENGTH: 1423
93 <212> TYPE: DNA
94 <213> ORGANISM: Mycobacterium smegmatis
96 <220> FEATURE:
97 <221> NAME/KEY: -10_signal
98 <222> LOCATION: (323)..(328)
99 <223> OTHER INFORMATION: putative promoter
101 <220> FEATURE:
102 <221> NAME/KEY: CDS
103 <222> LOCATION: (499)..(1134)
104 <223> OTHER INFORMATION: mspA-Gene
106 <220> FEATURE:
107 <221> NAME/KEY: RBS
108 <222> LOCATION: (492)..(496)
109 <223> OTHER INFORMATION: putative ribosome binding site
111 <400> SEQUENCE: 2
112 gttaacggag tcgggccgtc gatacggcgg cgaagatcat ccggcagatt ggcgcctggt 60
114 taaacccgcg taaacactgg taccgccggt ccgcgccgga aaaggttttg cctcacggtg 120
116 aatatgtgac ctgaattgca cttcacgggt aaaagcggag gtaaccgacg gttgccgcag 180
118 caccctcaca gcttgggcca aggtgacgtg cagcgcacgc ctgccggtgc cggatggcgg 240
120 tcaccgcaaa gtgtcaggca ctgccgaaag gtcagtcagc aaacttcact gcggctgtgg 300
122 tgcgaagtgc ggttgtggga cgtatccgtt gctgccgcgc ccctggcgt ttatgtttct 360
124 gctgccaact gtgagcgagg cattagagac agatgtgatc ctcttagatc tccgaagtct 420
126 ctgaacaggt gttgagccgg ttgcagacaa caaacaggt gggcctgagg ggccgccggc 480
128 gatacagtta gggagaac atg aag gca atc agt cgg gtg ctg atc gcg atg    531
129                Met Lys Ala Ile Ser Arg Val Leu Ile Ala Met
130                 1           5                       10
132 gtt gca gcc atc gcg gcg ctt ttc acg agc aca ggc acc tct cac gca    579
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/070,099

DATE: 08/12/2002
TIME: 17:41:50

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\08122002\J070099.raw

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133 Val Ala Ala Ile Ala Ala Leu Phe Thr Ser Thr Gly Thr Ser His Ala
134             15                  20                  25
136 ggc ctg gac aac gag ctg agc ctc gtt gat ggc cag gac cgc acc ctc   627
137 Gly Leu Asp Asn Glu Leu Ser Leu Val Asp Gly Gln Asp Arg Thr Leu
138         30                  35                  40
140 acc gtg cag cag tgg gac acc ttc ctc aat ggt gtg ttc ccc ctg gac   675
141 Thr Val Gln Gln Trp Asp Thr Phe Leu Asn Gly Val Phe Pro Leu Asp
142         45                  50                  55
144 cgc aac cgt ctt acc cgt gag tgg ttc cac tcc ggt cgc gcc aag tac   723
145 Arg Asn Arg Leu Thr Arg Glu Trp Phe His Ser Gly Arg Ala Lys Tyr
146 60                  65                  70                  75
148 atc gtg gcc ggc ccc ggt gcc gac gag ttc gag ggc acg ctg gaa ctc   771
149 Ile Val Ala Gly Pro Gly Ala Asp Glu Phe Glu Gly Thr Leu Glu Leu
150             80                  85                  90
152 ggc tac cag atc ggc ttc ccg tgg tcg ctg ggt gtg ggc atc aac ttc   819
153 Gly Tyr Gln Ile Gly Phe Pro Trp Ser Leu Gly Val Gly Ile Asn Phe
154             95                 100                 105
156 agc tac acc acc ccg aac atc ctg atc gac gac ggt gac atc acc gct   867
157 Ser Tyr Thr Thr Pro Asn Ile Leu Ile Asp Asp Gly Asp Ile Thr Ala
158         110                 115                 120
160 ccg ccg ttc ggc ctg aac tcg gtc atc acc ccg aac ctg ttc ccc ggt   915
161 Pro Pro Phe Gly Leu Asn Ser Val Ile Thr Pro Asn Leu Phe Pro Gly
162         125                 130                 135
164 gtg tcg atc tcg gca gat ctg ggc aac ggc ccc ggc atc cag gaa gtc   963
165 Val Ser Ile Ser Ala Asp Leu Gly Asn Gly Pro Gly Ile Gln Glu Val
166 140                 145                 150                 155
168 gca acg ttc tcg gtc gac gtc tcc ggc gcc gag ggt ggc gtg gcc gtg  1011
169 Ala Thr Phe Ser Val Asp Val Ser Gly Ala Glu Gly Gly Val Ala Val
170             160                 165                 170
172 tcg aac gcc cac ggc acc gtg acc ggt gcg gcc ggc ggt gtg ctg ctg  1059
173 Ser Asn Ala His Gly Thr Val Thr Gly Ala Ala Gly Gly Val Leu Leu
174         175                 180                 185
176 cgt ccg ttc gcc cgc ctg atc gcc tcg acc ggt gac tcg gtc acc acc  1107
177 Arg Pro Phe Ala Arg Leu Ile Ala Ser Thr Gly Asp Ser Val Thr Thr
178         190                 195                 200
180 tac ggc gaa ccc tgg aac atg aac tga ttcctggacc gccgttcggt        1154
181 Tyr Gly Glu Pro Trp Asn Met Asn
182         205                 210
184 cgctgagacc gcttgagatc ggcgcgtccc gctcccggtg tcgtcagctc atcgttgaca 1214
186 cgtgaactga cactcttcct agccggagcg kacgcgccga tcttgtgttc tgagcagttc 1274
188 tcagtccgtc cgccgcaaca ccagcgctga cggcgtacgc agcctgccca ccaccgcgcg 1334
190 ccagggacgc cccagcctgg gcaccacctc agcggtcggc acgatgcgcg gatcggtcac 1394
192 ctcgaacgtc tcaccgttca tcaccgcgc                                   1423
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 211
198 <212> TYPE: PRT
199 <213> ORGANISM: Mycobacterium smegmatis
201 <220> FEATURE:
202 <221> NAME/KEY: SIGNAL
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RAW SEQUENCE LISTING   DATE: 08/12/2002
PATENT APPLICATION: US/10/070,099   TIME: 17:41:50

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\08122002\J070099.raw

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203 <222> LOCATION: (1)..(27)
204 <223> OTHER INFORMATION: putative signal sequence of the MspA protein
206 <220> FEATURE:
207 <221> NAME/KEY: PEPTIDE
208 <222> LOCATION: (28)..(211)
209 <223> OTHER INFORMATION: mature MspA-protein
211 <400> SEQUENCE: 3
212 Met Lys Ala Ile Ser Arg Val Leu Ile Ala Met Val Ala Ala Ile Ala
213  1               5                  10                  15
215 Ala Leu Phe Thr Ser Thr Gly Thr Ser His Ala Gly Leu Asp Asn Glu
216             20                  25                  30
218 Leu Ser Leu Val Asp Gly Gln Asp Arg Thr Leu Thr Val Gln Gln Trp
219         35                  40                  45
221 Asp Thr Phe Leu Asn Gly Val Phe Pro Leu Asp Arg Asn Arg Leu Thr
222      50                  55                  60
224 Arg Glu Trp Phe His Ser Gly Arg Ala Lys Tyr Ile Val Ala Gly Pro
225  65                  70                  75                  80
227 Gly Ala Asp Glu Phe Glu Gly Thr Leu Glu Leu Gly Tyr Gln Ile Gly
228                 85                  90                  95
230 Phe Pro Trp Ser Leu Gly Val Gly Ile Asn Phe Ser Tyr Thr Thr Pro
231             100                 105                 110
233 Asn Ile Leu Ile Asp Asp Gly Asp Ile Thr Ala Pro Pro Phe Gly Leu
234         115                 120                 125
236 Asn Ser Val Ile Thr Pro Asn Leu Phe Pro Gly Val Ser Ile Ser Ala
237      130                 135                 140
239 Asp Leu Gly Asn Gly Pro Gly Ile Gln Glu Val Ala Thr Phe Ser Val
240 145             150                 155                 160
242 Asp Val Ser Gly Ala Glu Gly Gly Val Ala Val Ser Asn Ala His Gly
243             165                 170                 175
245 Thr Val Thr Gly Ala Ala Gly Gly Val Leu Leu Arg Pro Phe Ala Arg
246             180                 185                 190
248 Leu Ile Ala Ser Thr Gly Asp Ser Val Thr Thr Tyr Gly Glu Pro Trp
249         195                 200                 205
251 Asn Met Asn
252      210
258 <210> SEQ ID NO: 4
259 <211> LENGTH: 558
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: description of the artificial sequence: synthetic
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(558)
269 <223> OTHER INFORMATION: synmspA-Gene
271 <400> SEQUENCE: 4
272 atg ggc ctg gac aac gaa ctg tcc ctg gtt gac ggc cag gac cgt acc    48
273 Met Gly Leu Asp Asn Glu Leu Ser Leu Val Asp Gly Gln Asp Arg Thr
274  1               5                  10                  15
```

```
276 ctg acc gtt cag cag tgg gac acc ttc ctg aac ggt gtt ttc ccg ctg     96
277 Leu Thr Val Gln Gln Trp Asp Thr Phe Leu Asn Gly Val Phe Pro Leu
278         20                  25                  30
280 gac cgt aac cgt ctg acc cgt gaa tgg ttc cac tcc ggt cgt gcg aaa     144
281 Asp Arg Asn Arg Leu Thr Arg Glu Trp Phe His Ser Gly Arg Ala Lys
282         35                  40                  45
284 tac atc gtt gcg ggt ccg ggt gcg gac gag ttc gaa ggt acc ctg gaa     192
285 Tyr Ile Val Ala Gly Pro Gly Ala Asp Glu Phe Glu Gly Thr Leu Glu
286         50                  55                  60
288 ctg ggt tac cag atc ggc ttc ccg tgg tcc ctg ggt gtt ggt atc aac     240
289 Leu Gly Tyr Gln Ile Gly Phe Pro Trp Ser Leu Gly Val Gly Ile Asn
290 65                  70                  75                  80
292 ttc tct tac acc acc ccg aac atc ctg atc gac gac ggt gac atc acc     288
293 Phe Ser Tyr Thr Thr Pro Asn Ile Leu Ile Asp Asp Gly Asp Ile Thr
294                 85                  90                  95
296 gct ccg ccg ttc ggt ctg aac tct gtt atc acc ccg aac ctg ttc ccg     336
297 Ala Pro Pro Phe Gly Leu Asn Ser Val Ile Thr Pro Asn Leu Phe Pro
298         100                 105                 110
300 ggt gtt tct atc tct gct gat ctg ggc aac ggt ccg ggt atc cag gaa     384
301 Gly Val Ser Ile Ser Ala Asp Leu Gly Asn Gly Pro Gly Ile Gln Glu
302         115                 120                 125
304 gtt gct acc ttc tct gta gac gtc tct ggt gct gaa ggt ggt gtt gct     432
305 Val Ala Thr Phe Ser Val Asp Val Ser Gly Ala Glu Gly Gly Val Ala
306     130                 135                 140
308 gtt tct aac gct cac ggc acc gtt acc ggt gcg gct ggc ggt gtt ctg     480
309 Val Ser Asn Ala His Gly Thr Val Thr Gly Ala Ala Gly Gly Val Leu
310 145                 150                 155                 160
312 ctg cgt ccg ttc gct cgt ctg atc gct tct acc ggt gac tct gtt acc     528
313 Leu Arg Pro Phe Ala Arg Leu Ile Ala Ser Thr Gly Asp Ser Val Thr
314                 165                 170                 175
316 acc tac ggt gaa ccg tgg aac atg aac tga                             558
317 Thr Tyr Gly Glu Pro Trp Asn Met Asn
318         180                 185
322 <210> SEQ ID NO: 5
323 <211> LENGTH: 185·
324 <212> TYPE: PRT
325 <213> ORGANISM: artificial sequence
327 <220> FEATURE:
328 <221> NAME/KEY: PEPTIDE
329 <222> LOCATION: (1)..(184)
330 <223> OTHER INFORMATION: rMspA
332 <220> FEATURE:
333 <223> OTHER INFORMATION: description of the artificial sequence: synthetic
335 <400> SEQUENCE: 5
336 Met Gly Leu Asp Asn Glu Leu Ser Leu Val Asp Gly Gln Asp Arg Thr
337 1               5                   10                  15
339 Leu Thr Val Gln Gln Trp Asp Thr Phe Leu Asn Gly Val Phe Pro Leu
340         20                  25                  30
342 Asp Arg Asn Arg Leu Thr Arg Glu Trp Phe His Ser Gly Arg Ala Lys
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VERIFICATION SUMMARY   DATE: 08/12/2002
PATENT APPLICATION: US/10/070,099   TIME: 17:41:51

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\08122002\J070099.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date